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GenCore version 5.1.5  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model  
Run on: June 1, 2003, 15:19:59 ; Search time 4955.25 Seconds  
(without alignments)  
11622.905 Million cell updates/sec

Title: US-09-625-573-3  
Perfect score: 1979  
Sequence: 1 CAGCACTGCGTAGACAGC.....ATATGCAATATAAATTAG 1979

Scoring table: IDENTITY\_NUC  
Gapop 1.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: qb\_ba:\*

2: qb\_htg:\*

3: qb\_in:\*

4: qb\_om:\*

5: qb\_ov:\*

6: qb\_pat:\*

7: qb\_ph:\*

8: qb\_pl:\*

9: qb\_pr:\*

10: qb\_ro:\*

11: qb\_sts:\*

12: qb\_sy:\*

13: qb\_un:\*

14: qb\_vt:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_nv:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vt:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htg\_mus:\*

34: em\_htg\_pln:\*

35: em\_htg\_rnd:\*

36: em\_htg\_man:\*

37: em\_htg\_vrt:\*

38: em\_sy:\*

39: em\_htg\_hum:\*

40: em\_htg\_mus:\*

41: em\_htg\_other:\*

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1979	100.0	1979	6	AR116075	AR116075 Sequence 3
2	1979	100.0	1979	6	IT9543	IT9543 Sequence 3
3	1979	100.0	1979	9	U03905	Human monoc
4	1943.8	98.2	5471	9	HSNCPA02	HSNCPA02 Sequence
5	1943.8	98.2	143068	6	AX335952	AX335952 Sequence
6	1943.8	98.2	143068	9	U95626	U95626 Homo sapi
7	1942.2	98.1	185437	9	AC098613	AC098613 Homo sapi
c	8	1702	86.0	2900	2	AC087602
c	9	1313	66.3	10528	6	AX345236
c	10	1286.4	65.0	10528	6	AX345237
c	11	1231.4	62.2	1651	9	HSNCPIREC
c	12	1083	54.7	1083	6	AX232508
c	13	1081.4	54.6	1083	6	AX232506
c	14	1081.4	54.6	1083	9	HUMCPIR
c	15	1079.8	54.6	1083	6	AX280849
c	16	1078.2	54.5	1083	6	E13909
c	17	1023.8	51.7	1083	9	AF013958
c	18	980	49.5	2232	6	AR116074
c	19	980	49.5	2232	6	I7954.2
c	20	980	49.5	2232	9	HSU03882
c	21	780.6	39.4	1364	10	MM051717
c	22	777.4	39.3	2992	10	MM056819
c	23	775.8	39.2	1245	10	MMU17035
c	24	769.8	38.9	1365	10	RNU7349
c	25	712.6	36.0	1075	9	AF019379
c	26	711.8	36.0	1086	9	UB3324
c	27	711.8	36.0	1086	9	CAU83125
c	28	711	35.9	1059	9	AF035222
c	29	711	35.9	1059	9	AF081577
c	30	710.2	35.9	1130	9	AF291669
c	31	709.4	35.8	1059	9	AF075448
c	32	708	35.8	1966	9	MMU77672
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c	36	707.8	35.8	1059	9	AF141641
c	37	707.8	35.8	1059	9	AF212101
c	38	707.8	35.8	1059	9	AF349682
c	39	706.6	35.7	1059	9	AF075443
c	40	706.6	35.7	1059	9	AF075445
c	41	706.6	35.7	1059	9	AF177890
c	42	706.6	35.7	1059	9	AF177892
c	43	706.2	35.7	1059	9	AF005662
c	44	706.2	35.7	1059	9	AF035223
c	45	706.2	35.7	1059	9	AF051905

## ALIGNMENTS

RESULT 1	AR116075	AR116075	1979 bp	DNA
LOCUS		Sequence 3	from patent US 6132987.	
DEFINITION				
ACCESSION	AR116075	AR116075	GI:14096397	
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
				Unclassified.
				1 (bases 1 to 1979)
REFERENCE				
AUTHORS				Charo, I.F. and Coughlin, S.R.
TITLE				Recombinant mammalian monocyte chemotactic protein-1 (MCP-1)
JOURNAL				receptors (MCP-1R, CCR-2)
				Patent: US 6132987-A 3 17-OCT-2000;

Pred. No. is the number of results predicted by chance to have a

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		/organism="unknown"
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Matches 1979; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY 1 CAGGACTGGCTGAGACAAGCCACACAGTGAACAGAGAAAGTGGATGAACAGGAGCAT 60	Db 961	GGATGACTACTGGCTGACATCAATCCCATCATCTATGCCCTTCGTTGGGAGAAAGTTGAGAA 1020
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QY 61 TTCCCCAGTACATCACACACATGGTGCACATCTGGTTATCGAAATAACCA 120	Db 1021	GGATGACTCTCGGTGTTCTCCGAAAGCACATCACCAAGGCCTTCACATGGCTGAGAAAGTTGAGAA 1080
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Db 121 ACCAGAGGGTGTGAGAACACTACCCACCTTTGATTAGGTGTTACAGGTGCTCCGTACATA 180	Db 1081	TTTCTACAGGGAGACAGCTGGATGAGTGACTTCACAAACAGCCTTCACATGGCTGAGAAAGTTGAGAC 1140
QY 181 AATTGTAGCTGAGCAAATGGGCCAACACTCTGCCCTCGCTACTCGCTGGTTCA 240	Db 1141	AGGAAGTCGGTGGTTATAAACAGGAGGAGCTTGAATTGGTTATAAAAGGAGAA 1200
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QY 241 TCTTGTGTTTGTGGCAACACGCTGGTGTCTCATCTTAACACTGAAAGCTCA 300	Db 1201	TAACAACTGTGTTATAAACACACTTCAGGGAGCTTGAACATAGAACATGAAAGCTTAAAG 1260
Db 241 TCTTGTGTTTGTGGCAACACGCTGGTGTCTCATCTTAACACTGAAAGCTCA 300	Db 1201	TAACAACTGTGTTATAAACACACTTCAGGGAGCTTGAACATAGAACATGAAAGCTTAAAG 1260
QY 301 AGTGCTTGACATGACATTTACCTGCTCAACCTGCCCATCTGATCTGCTGTTCTTATA 360	Qy 1261	CAGGTGCCAGAACCTCAGGGCTGTTCTGAGACTATGCTCCAAAGCTCCATAGCTCCAG 1320
Db 301 AGTGCTTGACATGACATTTACCTGCTCAACCTGCCCATCTGATCTGCTGTTCTTATA 360	Db 1261	CAGGTGCCAGAACCTCAGGGCTGTTCTGAGACTATGCTCCAAAGCTCCATAGCTCCAG 1320
Qy 361 CTCTCCCATTGGGGCTACACTCTGCTGCAAAAGTGGCTTTGGGAATGGCAATGTCGA 420	Qy 1321	TCCAACATGTGCTCAGGAAATACTCCAGAAATTCGAAATACTGCTGAGCTTGTGAGAC 1380
Db 361 CTCTCCCATTGGGGCTACACTCTGCTGCAAAAGTGGCTTTGGGAATGGCAATGTCGA 420	Db 1321	TCCAACATGTGCTCAGGAAATACTCCAGAAATTCGAAATACTGCTGAGCTTGTGAGAC 1380
Qy 421 AATTATTCACAGGGCTGATCACATCGTTTACATCGTTTACATCGCTCAACCTGCCCA 480	Qy 1381	AAAGCCTCATCTCGCTCTGAAAAAATGCCATTAACCTTGTCTAACTCTCTTCTGAGCTTGTGAGCT 1440
Db 421 AATTATTCACAGGGCTGATCACATCGTTTACATCGTTTACATCGCTCAACCTGCCCA 480	Db 1381	AAAGCCTCATCTCGCTCTGAAAAAATGCCATTAACCTTGTCTAACTCTCTTCTGAGCTTGTGAGCT 1440
Qy 481 TGACATCGTGAATGACTCGCTTATGTCATGCTGTTGCTTTAAAGCCAGGACGG 540	Qy 1441	TCTTCTATAAATTCTACTCTCATCTGATCTGCTGAGCTTGTGAGCTTGTGAGCTTGTGAGCT 1500
Db 481 TGACATCGTGAATGACTCGCTTATGTCATGCTGTTGCTTTAAAGCCAGGACGG 540	Db 1441	TCTTCTATAAATTCTACTCTCATCTGATCTGCTGAGCTTGTGAGCTTGTGAGCTTGTGAGCT 1500
Qy 541 TCACCTTGGGGTGTGTTGACAGTGTGATCACCTGGTGTGGCTGTTGCTGTC 600	Qy 1501	TGGAGTGTGAAAGAAATGTGACAGGCCACAGTGAATGGGAGTGGGATGTGGGTCT 1560
Db 541 TCACCTTGGGGTGTGTTGACAGTGTGATCACCTGGTGTGGCTGTTGCTGTC 600	Db 1501	TGGAGTGTGAAAGAAATGTGACAGGCCACAGTGAATGGGAGTGGGATGTGGGTCT 1560
Qy 601 CAGGAAATCATTTACTAAATGCCAGAAACAGATCTGTTATGCTGTTGCCCTTAT 660	Qy 1561	AGGGCTGAGGGAGGGAGGACATGAGCATGCTGCTGAGCAAAAGCAAAAGT 1620
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Qy 661 TTCCACGAGGATGGATAATTCCACACATAATGAGACATTTGGGCTGGCTCTGC 720	Qy 1621	GAGCAAGGGCTCAGGCATTCACAGGAGTGGAAACTGGCTTCTGAGCTTGTGAGCT 1680
Db 661 TTCCACGAGGATGGATAATTCCACACATAATGAGACATTTGGGCTGGCTCTGC 720	Db 1621	GAGCAAGGGCTCAGGCATTCACAGGAGTGGAAACTGGCTTCTGAGCTTGTGAGCT 1680
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Qy 781 ACGAGAAAGGCTACATGGCAACTGGCAACTGGCAACTGGCAACTGGCAACTGG 840	Qy 1741	GGAGTTTGCTGGAGGCTCCGATGATCTCTTGTGAGCTAATGGCTGAGCTTGTGAGCT 1800
Db 781 ACGAGAAAGGCTACATGGCAACTGGCAACTGGCAACTGGCAACTGGCAACTGG 840	Db 1741	GGAGTTTGCTGGAGTCCGATGATCTCTTGTGAGCTAATGGCTGAGCTTGTGAGCT 1800
Qy 841 TCTTCTGGACTCCCTATACATGTCATCTGGTCAACCTGGCAACTGGCAACTGG 900	Qy 1801	ATTACAGTTTATGCTGGACCATGGCTTCTGAGCTTATGAAATATGCTGTT 1860
Db 841 TCTTCTGGACTCCCTATACATGTCATCTGGTCAACCTGGCAACTGGCAACTGG 900	Db 1801	ATTACAGTTTATGCTGGACCATGGCTTCTGAGCTTATGAAATATGCTGTT 1860
Qy 901 TGAGTAACGTGAAAAGCACACACTGGCAACAGGCAAGCCAACTGGCAACTGG 960	Qy 1861	CCATTGTTCAAGTGTCTTAGGCACATCCCTGCTGAGCTTCTGAGCTTATGCTGTT 1920
Db 901 TGAGTAACGTGAAAAGCACACACTGGCAACAGGCAAGCCAACTGGCAACTGG 960	Db 1861	CCATTGTTCAAGTGTCTTAGGCACATCCCTGCTGAGCTTCTGAGCTTATGCTGTT 1920

RESULT 2  
I79543  
LOCUS

1979 bp - DNA, linear

PAT 10-JUN-1998

SEQUENCE DEFINITION		Sequence 3 from patent US 5707815.	
INVENTION	17943	INVENTION	17953.1
REFERENCE	Charo, I.F. and Coughlin, S.R.	REFERENCE	ACGAGAAGAGGAGGATAGGGCAGTGGAGACTCATCTTCACCATGATGTTACCTTC
AUTHORS	Mammalian monocyte chemoattractant protein receptors and assays using them	AUTHORS	940
TITLE	Patent: US 5707815-A 3 13-JAN-1998;	TITLE	900
JOURNAL	Location/Qualifiers	JOURNAL	900
SOURCE	/organism="unknown"	SOURCE	900
BASE COUNT	530 a	BASE COUNT	530 a
ORIGIN	435 c	ORIGIN	451 g
Query Match	100.0% ; Score: 1919 ; DB: 6 ; Length: 1979;	Query Match	100.0% ; Score: 1919 ; DB: 6 ; Length: 1979;
Best Local Similarity	100.0% ; Pred. No: 0 ; Gaps: 0 ;	Best Local Similarity	100.0% ; Pred. No: 0 ; Gaps: 0 ;
Matches 1979; Conservative 0; Mismatches 0; Indels 0;	Matches 1979; Conservative 0; Mismatches 0; Indels 0;	Matches 1979; Conservative 0; Mismatches 0; Indels 0;	Matches 1979; Conservative 0; Mismatches 0; Indels 0;
1 CAGGACTGCTGAGACANGCCAAACAGCTGAAAGAGAAAGTGGATTGACAAGGAGCCT	1 CAGGACTGCTGAGACANGCCAAACAGCTGAAAGAGAAAGTGGATTGACAAGGAGCCT	1 CAGGACTGCTGAGACANGCCAAACAGCTGAAAGAGAAAGTGGATTGACAAGGAGCCT	1 CAGGACTGCTGAGACANGCCAAACAGCTGAAAGAGAAAGTGGATTGACAAGGAGCCT
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1 CAGGACTGCTGAGACANGCCAAACAGCTGAAAGAGAAAGTGGATTGACAAGGAGCCT	61 TTCCCCAGTACATCCACACATGCTGTCACATCTCGTCTCGTTTACAGAAATAACCA	61 TTCCCCAGTACATCCACACATGCTGTCACATCTCGTCTCGTTTACAGAAATAACCA	61 TTCCCCAGTACATCCACACATGCTGTCACATCTCGTCTCGTTTACAGAAATAACCA
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Qy	1861	CCATTGGTCAGATGCTTCTTAGGCCACATCCCCCTGTCTAAAAATTCAAGAAATTTCGTGTTTGT 1920
Db	1861	CCATTGGTCAGATGCTTCTTAGGCCACATCCCCCTGTCTAAAAATTCAAGAAATTTCGTGTTTGT 1920
Qy	1921	TATATAAAAGATGATTATCTATGATATGCTTAATATGATATGATATGCAATAATAAAATTAG 1979
Db	1921	TATATAAAAGATGCTTCTATGATATGCTTAATATGATATGCAATAATAAAATTAG 1979
RESULT	3	
LOCUS	HSU03905	
DEFINITION	HSU03905	1979 bp mRNA linear receptor (MCP-1RB)
ACCESSION	U03905	alternatively spliced mRNA, complete cds.
VERSION	U03905.1	GI:472557
KEYWORDS		
SOURCE		
ORGANISM	Homo sapiens	human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
1 (bases 1 to 1979)		
REFERENCE		
AUTHORS	Charo, I.F., Myers, S.J., Herman, A., Franci, C., Connolly, A.J. and	
Connolly, S.R.		
TITLE		molecular cloning and functional expression of two monocyte
JOURNAL		chemoattractant protein 1 receptors reveals alternative splicing of
MEDLINE	94195821	the carboxyl-terminal tails
PUBMED	8146186	proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)
REFERENCE		2 (bases 1 to 1979)
AUTHORS	Myers, S.J.	
TITLE		Direct Submission
JOURNAL		Submitted (02-DEC-1993) Scott J. Myers, Cardiovascular, The
FEATURES		Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110, USA
source		
Location/Qualifiers		
1.	1979	
/organism="Homo sapiens"		
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ANEWVFNAMCKLFLGFLYHIGFGGFLFQFLUTIDYLFLAVNEFLPKWAHS		
SVITWLVAVAFASVPGILIFTKCOKEDSVYVCGPYFPGNNNHFIMRNJGLVPLLMM		
VICYSGLIKLILCRNEKRRHARVTFITMVFILWTPYNTVILNNEQEEFGLSL		
CESTQSDQATQTYTGLMTCINPITIYAFVGEKFRRLSVFFRKHKITRKFCQCP		
530	a	FYRETVDGVSTNTPSNGQEVSAGL
BASE COUNT	435	c 451 g 563 t
ORIGIN		
Query Match	100.0%	Score 1979; DB 9; Length 1979;
Best Local Similarity	100.0%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
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Db	1	CAGGACTGCTTGAGAACGCCAACAGTGTCTAAAAATTCAAGAAATTGATTGAAACAGGACCCAT 60
Qy	61	TTCCCGAGTACATCCACAAATGCTGTCACATCTCGTTCTCGGTTATCAGAAATCCA 120
Db	61	TTCCCGAGTACATCCACAAATGCTGTCACATCTCGTTCTCGGTTATCAGAAATCCA 120
Qy	61	TTCCCGAGTACATCCACAAATGCTGTCACATCTCGTTCTCGGTTATCAGAAATCCA 120
Db	61	TTCCCGAGTACATCCACAAATGCTGTCACATCTCGTTCTCGGTTATCAGAAATCCA 120





QY	87	TCCACATCTGGTTCTGGTTTATCAGAAATACCAACGAGCGGTGAAGAGTCAACCC	146		Db	47192	GAGGAGCAGTTGATGTTGTTGTTAAGGGAGATAACAACTGATATAACAAACT	47251
Db	46112	TCCATATCCTGGTTCTGGTTTATCAGAAATACCAACGAGCGGTGAAGAGTCAACCC	46171		Qy	1227	TCAAGGGGTTTGTGACAATAGAACCTGTAAGCAGTGGCCAGAACCTCAGGGCTGT	1286
Qy	147	TTTTTGATPATGATTACGGTGCCTCCGTATATAATTGAGCTGAAGCAAATGGCCC	206		Db	47252	TCAAGGGTTTGTGACAATAGAACCTGTAAGCAGTGGCCAGAACCTCAGGGCTGT	47311
Db	46172	TTTTTGATPATGATTACGGTGCCTCCGTATATAATTGAGCTGAAGCAAATGGCCC	46231		Qy	1287	GTTGACTAATACAGACTATGTCACCCAAATGCAATCCAACTGTCAGGGAAATACTC	1346
Qy	207	CAACTCTGCTCCGCTCACTACTCGCTGGTTCACTTGTGTTGGCAACATGCTG	266		Db	47312	GTTGACTAATACAGACTATGTCACCCAAATGCAATCCAACTGTCAGGGAAATACTC	47371
Db	46232	CAACTCTGCTCCGCTCACTACTCGCTGGTTCACTTGTGTTGGCAACATGCTG	46291		Qy	1347	AGAAAACACTGTTGGTAGAGACTTTGACTCTCCAGAAGCTCATTCAGCTCCTGAAATA	1406
Qy	267	GTGTCCTCATCTTAATTAACCTGAAAGTGCAGTCAATTACCTGCTC	326		Db	47372	AGAAAACACTGTTGGTAGAGACTTTGACTCTCCAGAAGCTCATTCAGCTCCTGAAATA	47431
Db	46292	GTGTCCTCATCTTAATTAACCTGAAAGTGCAGTCAATTACCTGCTC	46351		Qy	1407	GCCATTACCTGTTGCTTAATCTCTTCTAGTCATATACTTCACCTCAATCTC	1466
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Qy	387	GCAATGGAAATTATTCAGGGTGTGGTAACTGGCTGTATCACATC	446		Db	47792	TGATTCCTCATGTTGCTGAATAAGGCCATTGAGGTAAAGAGAAATGTGACAG	47551
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Qy	507	GTCATGCTGTTGGCTTAAAGGCCAGGGGGTACCTTGGTGTGACAAGTGTG	566		Db	47612	ATGAGCATGGCTGAGCCMGGACAAAGAACCTGAGCAAAAGCTCAGCATTAGCCA	47671
Db	46532	GTCATGCTGTTGGCTTAAAGGCCAGGGGTCACTTGGGGTGTGACAAGTGTG	46591		Qy	1647	GGAGTATACTGTTGCTCATGCCCCATCTGCCACGTGTTAACCTGAGGTTCACC	1796
Qy	567	ATCACCTGGTTGTTGGCTGTTGGCTGTTGGCTCATCTGGTGTGACAAGTGTG	626		Db	47762	GGAGTATACTGTTGCTCATGCCCCATCTGCCACGTGTTAACCTGAGGTTCACC	47731
Db	46592	ATCACCTGGTTGTTGGCTGTTGGCTGTTGGCTCATCTGGTGTGACAAGTGTG	46651		Qy	1707	AGGTCAGGGAGGGTTGGAACTCTCAATAACCTGGAGTTGGTGTGACTCCGATGATC	1766
Qy	627	AAAGAAGATTCTGTTATGCTGCTTGGCTTATTTCCAGGGATGGAAATACTCCAC	686		Db	47732	AGGTCAGGGGAGGTTGGAAACTGCAATAACCTGGAGTTGGTGTCTAGGTGATC	47791
Db	46652	AAAGAAGATTCTGTTATGCTGCTTGGCTTATTTCCAGGGATGGAAATACTCCAC	46711		Qy	1767	TCTTTGCTATAAGTCATGACATATTGCTTATTACAGTTATCTAGTCAGTGTGACCCG	1826
Qy	687	ACATAAAGGAGACATTGGGCTCTGGCTCATCTGGCTCATCTGGCTCATCTGGCT	746		Db	47792	TCTTTGCTATAAGTCATGACATATTGCTTATTACAGTTATCTAGTCAGTGTGACCCG	47851
Db	46712	ACATAAAGGAGACATTGGGCTCTGGCTCATCTGGCTCATCTGGCTCATCTGGCT	46771		Qy	1827	CACCTTACATTGAAATCTGATGAAATACTGTCATGTTGAGTGTCTAGTCAGTGTGACCCG	1886
Qy	747	TGGGAATTCCTGAAACCTGCTGGCTCTGGCTCATCTGGCTCATCTGGCT	806		Db	47852	CACCTTACATTGAAATCTGTCATGTTGAGTGTCTAGTCAGTGTGACCCG	47911
Db	46772	TGGGAATTCCTGAAACCTGCTGGCTCATCTGGCTCATCTGGCTCATCTGGCT	46831		Qy	1887	CATCCCCCTCTCTAAATTCAGAAAAATTTCAGTTTATAAAAGTCATTCTATGATA	1946
Qy	807	AGAGTCATCTTACCATCATGATGTTACTCTCTGGACTCCCTATACTCTTC	866		Db	47912	CATCCCCCTCTCTAAATTCAGAAATTGCTTGTGTTTATAAAAGTCATTCTATGATA	47971
Db	46832	AGAGTCATCTTACCATCATGATGTTACTCTGGACTCCCTATAACATCTTC	46691		Qy	1947	TGCTTATATGTTATGCAATATAAA	1973
Qy	867	ATTCCTGAAACCTGCTGGCTGATGTTACTCTGGACTCCCTATAACATCTTC	926		Db	47972	TGCTTATATGTTATGCAATATAAA	47998
Db	46892	ATTCCTGAAACCTGCTGGCTGATGTTACTCTGGACTCCCTATAACATCTTC	46951		RESULT	6		
Qy	927	CTGGACCAAGCCACGGTACAGACTCTGGATGACTCTGCTGATCAATCCC	986		LOCUS	HSU95626	143068 bp	DNA
Db	46952	CTGGACCAAGCCACGGTACAGACTCTGGATGACTCTGCTGATCAATCCC	47011		SOURCE	Homo sapiens	Linear	PRI 16 MAY 1997
Qy	987	ATCACCTATGCCCTGGTGGGAGAGTTCAGAAAGTTCTCCGAAAG 1046		DEFINITION	Homo sapiens ccr2b (ccr2), cor2a (ccr2), ccr5 (ccr5) and cor6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.			
Db	47012	ATCACCTATGCCCTGGTGGGAGAGTTCAGAAAGTTCTCCGAAAG 47071		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
Qy	1047	CACATCAAGCCAGCTCTGGCTCATCTGGCTCATCTGGCTCATCTGGCT	1106		REFERENCE	1 (bases 1 to 143068)		
Db	47072	CACATCAAGCCAGCTCTGGCTCATCTGGCTCATCTGGCTCATCTGGCT	47131		AUTHORS	McCombie, W.R., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Nhan, M., Parnell, L., Dedhia, N., Ansari, A., Mardis, E., Schutte, K., Gnoj, L., de la Bastide, M., Kaplan, N., Greco, T., Touchman, J.,		
Qy	1107	GTGACTTCAAAACAGCCCTTCAGCTGGAGAGTTCAGGGAGCTGGCTGTTTATAAAAC	1166					
Db	47132	GTGACTTCAAAACAGCCCTTCAGCTGGAGAGTTCAGGGAGCTGGCTGTTTATAAAAC	47191					
Qy	1167	GAGGAGCAGTTGATGTTGTTGTTATAAAAGGGAGATAACATCTGATATAACAAACT	1226					

Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., DeSilva, M., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.	JOURNAL Human BAC clone 110P12 Unpublished (1997) 2 (bases 1 to 143068)	REFERENCE McCombie, R.W., Wilson, R., Chen, E., Gibbs, R., Zuo, L., Johnson, D., Nhan, M., Parnell, L., Dehia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Basile, M., Kaplan, N., Greco, T., Touchman, J., Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., DeSilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.	AUTHORS Nhan, M., Parnell, L., Dehia, N., Ansari, A., Mardis, E., Schutz, K., Gnoj, L., de la Basile, M., Kaplan, N., Greco, T., Touchman, J., Muzny, D., Chen, C.-N., Evans, C., FitzGerald, M., See, L.H., Tang, M., Porcel, B.M., Dragan, Y., Giacalone, J., Pae, A., Powell, E., Solinsky, K.A., DeSilva, U., Diaz-Perez, S., Zhou, X., Yu, Y., Watanabe, M., Doggett, N., Garcia, D. and Sagripanti, J.-L.												
		COMMENT Regions with single-strand coverage are as follows:													
		<table border="1"> <tr> <td>31434 - 31443</td> <td>37900 - 37968</td> <td>53303 - 53357</td> </tr> <tr> <td>59166 - 59206</td> <td>63708 - 63998</td> <td>65200 - 65335</td> </tr> <tr> <td>78605 - 78715</td> <td>92135 - 92137</td> <td>112377 - 112551</td> </tr> <tr> <td>112778 - 11284</td> <td>134284 - 134309</td> <td>134914 - 135019</td> </tr> </table>	31434 - 31443	37900 - 37968	53303 - 53357	59166 - 59206	63708 - 63998	65200 - 65335	78605 - 78715	92135 - 92137	112377 - 112551	112778 - 11284	134284 - 134309	134914 - 135019	
31434 - 31443	37900 - 37968	53303 - 53357													
59166 - 59206	63708 - 63998	65200 - 65335													
78605 - 78715	92135 - 92137	112377 - 112551													
112778 - 11284	134284 - 134309	134914 - 135019													
FEATURES	source	Location/Qualifiers													
		1. .143068 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="13" /clone="BAC 110P12" /gene="ccr2" /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) mRNA (Accession Number U80924), two alternatively spliced mRNAs." join(46056, .47046, 48255. .49505) /gene="ccr2" /product="ccr2a" /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced mRNA encoding A-form carboxyl tail, Accession Number U80924." 46056. .47987 /gene="ccr2" /product="ccr2b" /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced mRNA encoding B-form carboxyl tail. Accession Number: U80924." join(46106, .47046, 48255. .48438) /gene="ccr2" /note="confirmed by similarity to Human monocyte chemoattractant protein 1 receptor (ccr2) alternatively spliced A-form. Encoded by GenBank Accession Number U80924, 91.116965" /codon_start=1 /product="ccr2a" /protein_id="AAB57791.1" /db_xref="GI:2104518" /translation="MISRSSEPRINTNESGEVTFIDYDGAFCHEFDVKOQAGQI LPPFLSLVTFGFVNMLVFLINNKKLCLDIYLNLAISDLFLFTLPLWAHS ANERVEFGNMACKLEPTGGLYHIGYFGFVFLLTIDRYLAIVHAVEALKARTVTFGVV SVTFLVWAFASVSPGLIEPKOKEVDSVYCCPFPGWNNFETIMRNFLGIVLPEFL VICKSGILKLLRCNEKRRHRAVEITIMTMIVYFLWTFPVNVLNTQFEGFLSM CESTSQDQATQETLGLTHCCCLNPLIVAFVGKEERSLFLHALGCRAPLQPKVCGG PGYRGPKNWKVYTGQLLDPRGKGSSIGRAFEASLQDGKA"													
CDS															
CDS															





Mon Jun 2 09:42:08 2003

FEATURES

source

### Query Match

Best Local

Matches 19

5

2 / CL

הנִּזְמָן 11003

1000

87 **AC**

REFERENCE	RESULT 8	LOCUS	DEFINITION	AC087602/c	2900 bp	DNA	linear	HTG 08-MAR-2001
AUTHORS	OCUS	DEFINITION	Pan troglodytes clone RP43-177M18, ***	Pan troglodytes	Pan troglodytes	Pan troglodytes	SEQUENCING IN PROGRESS ***	
VERSION	VERSION	VERSION	AC087602.3	GI:14190646	HTGS_PHASE1	Pan troglodytes		
EPRINTS	EPRINTS	EPRINTS	AC087602	1 unorderded piece.	Pan troglodytes			
SOURCE	SOURCE	SOURCE						
ORGANISM	ORGANISM	ORGANISM						
Db	15143	GAGGAGCAGTTGATGTTGTTGAACTAGAAACCTGTAAGCAGGTAAACATCTGATATAAACAAACT	1526					
Qy	1227	TCAAGGGTTGTTGAACTAGAAACCTGTAAGCAGGTAAACCTCAGGGATACTCTAGGGCT	1226					
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Qy	1407	GCCTCATTAACCTGTGCTTAATCCCTTTGTTGTTAGCTTCAATTCTACTCAATCTC	1466					
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Qy	1467	TGATCTGCAATGCTGAAATCAGGGCCAGCTGGAGGTAAAGAGAATGTCAG	1526					
Db	15443	TGATCTGCAATGCTGAAATCAGGGCCAGCTGGAGGTAAAGAGAATGTCAG	15502					
Qy	1527	GCACAGATGAATGGGGATGGGGATAGTGGGGTCAGGCAGGAGAAGGGGAGAC	1586					
Db	15503	GCACAGATGAATGGGGATGGGGATAGTGGGGTCAGGCAGGAGAAGGGGAGAC	15562					
Qy	1587	ATGAGCATGGCTGACCCCTGACCAAAAGCTGACAAAGGGCTACGATTACGCCA	1646					
Db	15563	ATGAGCATGGCTGACCAAAAGCTGACAAAGGGCTACGATTACGCCA	15622					
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Db	15633	GGAGATGATACTGCTCTAGCCCTGACCTGGGAACCTGCAATACCTGGAGTTTGGGAGCTGAGGAGAAGGGGAGAC	15682					
Qy	1707	AGGTCAAGGAGAGGTTGGCAACCTGCAATACCTGGAGTTTGGGAGCTGAGGAGAAGGGGAGAC	1766					
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Qy	1947	TGCTATAATGTTATGCAATATA	1973					
Db	15923	TGCTATAATGTTATGCAATATA	15949					

Carron, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhardt, C., Edgar, D., Edwards, C.C., Elhai, C., Escott, M., Fallis, T., Ferrugato, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, L.R., Gorre, J.H., Cuevarra, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulky, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karovic, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureishi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, H., Li, J., Li, Z., Lichatowicz, O., Liu, C., Liu, J., Liu, W., Lousegod, L., Lozada, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, I.M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, E., McLeod, M.P., Meador, M., Mei, G., Netzker, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, M., Neal, D., Newton, J., Newtonson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokiekwo, S., Oghu, M., Okwunou, G., Ogunyemi, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Reit, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherzer, S., Scott, G., Shen, H., Shoshtari, N., Siisson, I., Sodergren, E., Sonakal, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svratek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Ver, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watling, M., Williams, G., Williamson, A., Wleczyc, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.	AL	Unpublished
	CE	2 (bases 1 to 2900)
	RS	Worley, K.C.
	AL	Direct Submission
	CE	Submitted (14-JAN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
	RS	3 (bases 1 to 2900)
	AL	Direct Submission
	CE	Submitted (08-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
	RS	Worley, K.C.
	AL	Submitted (08-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
	CE	Worley, K.C.
	RS	Sequencing vector: M13, L09821
	AL	Chemistry: Dye-primer Bodipy: 61% of reads
	CE	Chemistry: Dye-terminator Big Dye: 38% of reads
	RS	Contact: hgc-help@bcm.tmc.edu
	AL	Assembly program: Phrap; version 0.990329
	CE	Consensus quality: 15/17 bases at least Q40
	RS	Consensus quality: 28/63 bases at least Q30
	AL	Consensus quality: 43/61 bases at least Q20
	CE	Estimated insert size: 21502; sum-of-contigs estimation
	RS	Quality coverage: 0x in Q20 bases; agarose-fp estimation
	AL	Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation

\* consists of 1 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 2900: contig of 2900 bp in length.

1 .2900 Location/Qualifiers

/organism="Pan troglodytes"

/db\_xref="taxon:9598"

/clone="RP43-177M18"

BASE COUNT 808 a 656 c 633 g 803 t

ORIGIN

FEATURES	source	Query Match	Score	Length	DB	2:	Length	2900:
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QY	151	TGATTATTGATTAACGGCTCTGCTTACGGCTCTGCTTAAATTGAGCAATTTGGCCAAC	210					
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QY	211	TCTGCGCTCTACTCGCCTGCTCATCTTGGTTGGCAACATGCTGGTCG	270					
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QY	211	TCTCATCTTAATAACTGCAAAAGCTGAACTGCTTACCTGCTCAACC	330					
Db	2489	TCTCATCTGATAAACTGCAAAAGCTGAAAGCATACTGTATACCTGCTCAACC	2430					
QY	331	TGGCATCTCTGCTGCTTCTTACTCTCCATTGGCTTACTCTGCTGAA	390					
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QY	391	ATGAGTGGCTTGGGAATGCAATGCGAAATTATTCACAGGCTGTATACATGGT	450					
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QY	571	CCTGGTTGGCTGCTGTTGCTCTGTCCTCCAGGAATCATCTTACTAAATGCCAAG	630					
QY	691	TAATGAGGAACATTGGGGCTGCTGCTCATGGCTACTCTGCTACTCGG	750					
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QY	631	AAGATTCTGTTATGCTGGCCCTTATTCCAGGATGGATAATTCCACAA	690					
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AX345236	AX345236	10528 bp	DNA	Linear	PAT 01-FEB-2002
DEFINITION	Sequence 307 from Patent WO200928.				
ACCESSION	AX345236				
VERSION	AX345236.1				
KEYWORDS					
SOURCE	OLEK, A., Piepenbrock, C. and Berlin, K.				
ORGANISM	synthetic construct				
REFERENCE	1				
AUTHORS	OLEK, A., Piepenbrock, C. and Berlin, K.				
TITLE	Diagnosis of diseases associated with the immune system				
JOURNAL	Patent: WO 0200928-A 307 03-JAN-2002;				
FEATURES	Epigenomics AG (DE)				
source	Location/Qualifiers				
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BASE COUNT	3072 a	86 c	2419 g	4951 t	
ORIGIN					
Query Match Score 66.3%	Score 1313; DB 6; Length 10528;				
Best Local Similarity 79.7%;	Pred. No. 0;				
Matches 1550; Conservative 0;	Mismatches 395; Indels 0; Gaps 0;				
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Qy 89	CACACTCGPTCTCGSTTATAGAAATAACAGAGAAAGTGCACCCTT	148			
Db 8387	TATATTTCGTTTCGTTTATTAGAAATAACAGAGTTTATATTATGTT	8446			
Qy 149	TTTGTATTATGATGTTAGGTGCTCCCGTCAATAATTGACCTGAAATGGGCCA	208			
Db 8447	TTTGTATTATGATGTTAGGGTTTGTATAAATTGACCTGAAATGGCTTAA	8506			
Qy 209	ACTCTGCCTCCGCTACTCGCTGGTICATCTTGTGGCCAACATGCTGTT	268			
Db 8507	ATTATGTTCTGTTTATCGTGTGTTATGGTGTGTTATGTGTTG	8566			
Qy 269	CGTGCCTCATCTTAATAACTGCAAAAGTCAATTACCTGCTCAA	328			
Db 8567	CGTTTATTTATTAATAATGTTAAAGTGAAGGAAATGGCTTAA	8626			
Qy 329	CTGGCCATCTCATCTGTTGACTCTCCAAUTGTGGCTCACTCTGCTGC	388			
Db 8627	TTTGTATTCTCATCTGTTTATATTTTATATGTTGTTATGTGTT	8686			
Qy 389	AAATGAGTGGGTCTTGGGAATGCAAAATTATCACAGGGCTGTATCACATCG	448			
Db 8687	AAATGAGTGGGTCTTGGGAATGTAATGCTAAATTATGCTGTTATATCGG	8746			
Qy 449	TTATTGCGGAATCTCTCATCTCCTGCAATGATGATACTCTGGTATGTT	508			
Db 8747	TTATTGCGGAATTTTATTTTATTTTATGATGATGATGTTATGTGTT	8806			
Qy 509	CCATGCTGTTGCTTAAACGAGGCTTGGTGTGACAAGTGTGAT	568			
Db 8807	TTATGCTGTTGCTTAAACTAGACGGTATTGGGGTGTATAAGCTGAT	8866			
Qy 569	CACCTGGCTGGCTGCTGGTGTGCAAGGAATCATCTTACTAAATGCCAGA	628			
Db 8867	TATTGCTGTTGCTTAAATGTTAGGAAATTATGTTAGGAAATTTTAT	8926			
Qy 629	AGAAAGTCTGTTATGCTGCTGGTGTGCTGTCATCTGGCTCATCTGCTACTC	748			
Db 8927	AGAAAGTCTGTTATGCTGCTGGTGTGCTGTCATCTGGCTCATCTGCTACTC	688			
Qy 689	ATAATGAGGACATTGGGCTGGTGTGCTGTCATCTGGCTCATCTGCTACTC	9046			
Db 10067	TTTGTATAAAGTGTGTTTGGGCTGGTGTGCTGTCATCTGGCTCATCTGCTACTC	10126			



Db	641	ACATACATTAACCTAAACCAAAACAAAAAAACAAAAAAACTACNGCATTCAACAAAAA	582
Qy	1650	GATGATACTGGTCTTGTGCCCATGTGGCACCGTGTATTAACCTTGAAAGGTTCAACAGG	1709
Db	581	AATATACATTAATCTTAACCCCATCTACCACTGATATTAAACCTTAAAATTCACCAA	522
Qy	1710	TCTGGAGAGTTGGAACTGCAATAACCTGGAGTTGGTGGAGATCGATCTCTCT	1769
Db	521	TCTAAAAAATTTAAACATACATTAACCTTAAATTTAATCGATAATCT	462
Qy	1770	TTCGCAATAGTCGATGACATTTTCGCTTATACAGCTTATCTATGGCACCCATGGAC	1829
Db	461	TTTACATTAATATATATTTACTTTAATCAATTAACTATCTATCTATACCCATACAG	402
Qy	1830	CCTACATTGAAATCTATGAAATATCATGCTCCATTGTCAGATGCTCTTGGCACAT	1889
Db	401	CTTACATTAAATCTATAAATATCATACTCCATTATCAAAATACATCTTAAACCAT	342
Qy	1890	CCGCCCTGCTCTAAATTCAGAAATTTGGTTTATAAAAGATGCCATTATGATATGC	1949
Db	341	CCCTCTATCTAAATTCAGAAATTTGGTTTATAAAAGATGCCATTATGATATGC	282
Qy	1950	TATATATGATATGCAATATAAA	1973
Db	281	TAATATATATATACATATATAA	238
<b>RESULT 11</b>			
HSNC1P1REC			
LOCUS		HSNC1P1REC	
DEFINITION		1651 bp	mRNA
ACCESSION			linear
VERSION	X95583		PRI 03-MAP1
KEYWORDS	X95583.1 GI:4468944		mRNA for monocyte chemotactic protein-1 (MCP-1) receptor
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
VERSION			
TITLE			
REMARKS			
JOURNAL			
MEDLINE			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
Source			
Q86420			
741-1971		03882 nucleotides	981-1134
Location/Qualifiers			
1..1651			
/organism="Homo sapiens"			
/db_xref="taxon:9606"			
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/tissue_type="monocytic line"			
<1..1231			
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/standard_name="monocyte chemoattractant protein 1 receptor"			
/note="related to U03905"			
<1..423			
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/protein_id="CAA64835_1"			
/db_xref="GI:4468945"			
/translition="CAGGILKLTLLCRNEKRRRAVVRIFTIMIVFLFWTPYNIW			

QY	1641	CAGCCAGGAGATGATACTGGTCTTAAGCCCCATCTGCCACGTGTTAACCTTGAGGG	1700	QY	381	TCTGCTGCAAATGAGTGGTCTTGGGATGCAAATTACAGGGCTGTAT 440
Db	901	CAGCCAGGAGATGATACTGGTCTTAAGCCCCATCTGCCACGTGTTAACCTTGAGGG	960	Db	301	TCTGCTGCAAATGAGTGGTCTTGGGATGCAAATTACAGGGCTGTAT 360
QY	1701	TTCACCAAGTCAGGGAGAGTTGGGAACCTGCAATAACCTGGGAGTTGGTGAGTCGA	1760	QY	441	CACATCGTTATTTGGGGAAATCTCTCATATCCCTCTGAAATCGATACTGGCTGTAT 500
Db	961	TTCACCAAGTCAGGGAGAGTTGGGAACCTGCAATAACCTGGGAGTTGGTGAGTCGA	1020	Db	361	CACATCGTTATTTGGGGAAATCTCTCATATCCCTCTGAAATCGATACTGGCTGTAT 420
QY	1761	TGATTCTCTTTCATAGTCATGACATATTTCGCTTATACAGTTTATGGCA	1820	QY	501	GCTATTGTCATGGGTTGGCTTAAAGCZAGGACGTACCTTGGGGGGTGTGACA 560
Db	1021	TGATTCTCTTTCATAGTCATGACATATTTCGCTTATACAGTTTATGGCA	1080	Db	421	GCTATTGTCATGGGTTGGCTTAAAGCZGGACGTACCTTGGGGGGTGTGACA 480
QY	1821	CCCATGCACTTCATGAAATCTTATCATGCTCATGGCTCATCTTACTAA	1880	QY	561	AGTTGATACCTGGTGTGGCTGTTGCTGTTCTGTCAGGAATCATCTTACTAA 620
Db	1081	CCCATGCACTTCATGAAATCTTATCATGCTCATGGCTCATCTTACTAA	1140	Db	481	AGTTGATACCTGGTGTGGCTGTTGCTGTTCTGTCAGGAATCATCTTACTAA 540
QY	1881	AGGCCACATCCCCCTCATGAAATCTTATCATGCTCATGGCTCATCTTACTCT	1940	QY	621	TGCCAGAAAGAAGATTCTGTTTATGCTGGCCCTTATTTCCACGAGGATGGATAAT 680
Db	1141	AGGCCACATCCCCCTGCTTATCATGAAATCTTATCATGCTCATGGCTCATCTTACT	1200	Db	541	TGCCAGAAAGAAGATTCTGTTTATGCTGGCCCTTATTTCCACGAGGATGGATAAT 600
QY	1941	ATGATATGCTTAATATATGTTATGCAATTATAAA	1973	QY	681	TTCACACAAATTCAGGAACTTGGGACTCATTTGGGCTCTGTTGCTGTTCTGTCAGGAAGAGGCTAGG 740
Db	1201	ATGATATGCTTAATATATGTTATGCAATTATAAA	1233	Db	601	TTCACACAAATTCAGGAACTTGGGCTCTGTCAGGAAGAGGCTAGG 660
RESULT 12				QY	741	TGCTACTCGGAATCTGAAACCTGCTTCGGTGTGAAACGAGAAAGAGGCTAGG 800
LOCUS	AX232508	AX232508	1083 bp	Db	661	TGCTACTCGGGAACTCTGAAACCTGCTTCGGTGTGAAACGAGAAAGAGGCTAGG 720
DEFINITION	Sequence 3 from Patent WO0162796.			QY	801	GCAGTGAGAGTCATCTTCACCATCATGATGTTACTTTCTCTGGACTCCCTATAAC 860
ACCESSION	AX232508			Db	721	GCAGTGAGAGTCATCTTCACCATCATGATGTTACTTTCTCTGGACTCCCTATAAC 780
VERSION	AX232508.1	GI:15592570		QY	861	ATTGTCATTCUCCCTGAACTTCCAGGAATTCTGGCCTGCTGTCAGGAAGACCC 920
SOURCE	human.			Db	781	ATTGTCATTCUCCCTGAACTTCCAGGAATTCTGGCCTGCTGTCAGGAAGACCC 840
ORGANISM	Homo sapiens			QY	921	AGTCACATGGACCAAGCCACGGTACAGAGACTCTGGGATGACTCTGCTGATC 980
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				Db	841	AGTCACATGGACCAAGCCACGGTACAGAGACTCTGGGATGACTCTGCTGATC 900
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				QY	981	AATCCCATCATGCTATGCTCTGCTGGGAGAAAGTTCAGAAAGSTATCTCCTGTC 1040
REFERENCE	1 (bases 1 to 1033)			Db	901	AATCCCATCATGCTATGCTCTGCTGGGAGAAAGTTCAGAAAGSTATCTCCTGTC 960
AUTHORS	Valdes, A.M., Groot, P.H. and Spurr, N.K.			QY	1041	CGAAAGCACATCCAGGCTCTGCAACATGCGCTCTGCTGGGAGAGCTGGGT 1100
TITLE	Ccr-64, polymorphic variant of the human ccr2 receptor and its use in the diagnosis and treatment of atherosclerosis			Db	961	CGAAAGCACATCCAGGCTCTGCAACATGCGCTCTGCTGGGAGAGCTGGGT 1020
JOURNAL	Patent: WO 0162796-A 3 30-AUG-2001;			QY	1101	GATGGAGTGACTCAAGAACAGCCCTTCACGGGAGGAGCTGGGTGGGTTA 1160
FEATURES	SMITHKLINE BEECHAM PLC (GB)			Db	1021	GATGGAGTGACTCAAGAACAGCCCTTCACGGGAGGAGCTGGGTGGGTTA 1080
LOCATION/Qualifiers	1..1083			QY	1161	TAA 1163
ORGANISM	/organism="Homo sapiens"			Db	1081	TAA 1083
BASE COUNT	255 a	260 c	247 g	QY	1161	TAA 1163
ORIGIN				Db	1081	TAA 1083
Query Match	54.7%	Score 1083; DB 6; Length 1083;		RESULT 13		
Best Local Similarity	100.0%	Pred. No. 6.2e-287;		AX32506	AX32506	
Matches 1083;	Conservative 0;	Mismatches 0;		LOCUS	Sequence 1	from Patent WO0162796.
		Indels 0;		DEFINITION		
		Gaps 0;		ACCESSION	AX232506	
				VERSION	AX232506	
				KEYWORDS	GI:15592569	
				ORGANISM	Homo sapiens	
				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
				REFERENCE	1 (bases 1 to 1083)	
				AUTHORS	Valdes, A.M., Groot, P.H. and Spurr, N.K.	
				TITLE	Cor2-64, polymorphic variant of the human ccr2 receptor and its use in the diagnostic and treatment of atherosclerosis	

JOURNAL	Patent: WO 01627996-A 1 30-AUG-2001;	QY	981	AATCCCATCATCTATGCCCTTCGTTGGGAAAGTCAGAGGATCTCTCGTGTCTTC 1040
FEATURES	SMTHKLIN BEECHAM PLC (GB)	Db	901	AATCCCATCATCTATGCCCTTCGTTGGGAAAGTCAGAGGATCTCTCGTGTCTTC 960
source	Location/Qualifiers 1. /organism="Homo sapiens" /db_xref="taxon:9606"	QY	1041	CGAAGCACATCCAAGGCTTCTGCAAACAACTGTCAGTTTCTACAGGAGACAGTG 1100
BASE COUNT	256 a 260 C 246 g 321 t	Db	961	CGAAGCACATCCAAGGCTTCTGCAAACAACTGTCAGTTTCTACAGGAGACAGTG 1020
ORIGIN		QY	1101	GATGAGAGACTAACAAACCCCTTCACTGGAGGAACTGTCGGCTGGTTTA 1160
Query Match	54.6%; Score 1081.4; DB 6; Length 1083;	Db	1021	GATGAGAGACTAACAAACCCCTTCACTGGAGGAACTGTCGGCTGGTTTA 1080
Best Local Similarity	99.9%; Pred. No. 1.7e-286;	QY	1161	TAA 1163
Matches 1082; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		Db	1081	TAA 1083
Db	1 ATGTGTCCACATCTGTTCTCGTTATCAGAAATAACACAGAGGGTGAAGAGTC 140	RESULT 14		
QY	141 ACCACCTTTGATTATAGGTCTCCNGTCATAAATTGACCTGAAGAAATT 200	HUMMCP1R	1083 bp	mRNA
Db	61 ACCACCTTTGATTATAGGTCTCCNGTCATAAATTGACCTGAAGAAATT 120	LOCUS	Human mRNA for monocyte chemoattractant protein 1 receptor (MCP-1 receptor), complete cds.	linear
QY	201 GGGCCCCACTCCGCCGCCCTACTCGCTGTGTATCTTGGTTGGGCCAC 260	DEFINITION		PRI 23-JUN-1999
Db	121 GGGCCCCACTCCGCCGCCCTACTCGCTGTGTATCTTGGTTGGGCCAC 180	ACCESSION	D29984	
QY	261 ATGCTGGTGTCTCATCTTAATAACTCGAAAGCTCAACTGACATTAC 320	VERSION	1. GI:531246	
Db	181 ATGCTGGTGTCTCATCTTAATAACTCGAAAGCTCAACTGACATTAC 240	KEYWORDS	G-protein-coupled seven-transmembrane-type receptor; MCP-1 receptor; monocyte chemoattractant protein 1 receptor.	
QY	321 CTGCTCAACCTGGCCATCTCTGATCTGTCTTCTTCTTACTCTCCATGTGGCTCA 380	SOURCE		
Db	241 CTGCTCAACCTGGCCATCTCTGATCTGTCTTCTTACTCTCCATGTGGCTCA 300	ORGANISM	Homo sapiens	
QY	381 TCTGCTGCAAAATGAGTCGGTCTTGGAAATATTACAGGGCTGTAT 440	REFERENCE		
Db	301 TCTGCTGCAAAATGAGTCGGTCTTGGAAATATTACAGGGCTGTAT 360	AUTHORS	Yamagami,S., Tokuda,Y., Ishii,K., Tanaka,H. and Endo,N.	
QY	441 CACATCGGTATATTGGCGGAATCTCTCATCTGCAATCGATACCTG 500	TITLE		
Db	361 CACATCGGTATATTGGCGGAATCTCTCATCTGCAATCGATACCTG 420	JOURNAL		
QY	501 GCTATGTCATGCTGTGTTAAAGCAGGCGTCACTCTGTCAGGANTCATCTTACTAA 560	COMMENT		
Db	421 GCTATGTCATGCTGTGTTAAAGCAGGCGTCACTCTGTCAGGANTCATCTTACTAA 480	TITLE		
QY	561 AGTGTATCACTGGTGTGTTAAAGCAGGCGTCACTCTGTCAGGANTCATCTTACTAA 620	JOURNAL		
Db	481 AGTGTATCACTGGTGTGTTAAAGCAGGCGTCACTCTGTCAGGANTCATCTTACTAA 540	COMMENT		
QY	621 TGCCAGAAAGAGATCTGTTATGCTGTGGCCCTATTTCCAGAGATGGAATAAT 680	COMMENT		
Db	541 TGCCAGAAAGAGATCTGTTATGCTGTGGCCCTATTTCCAGAGATGGAATAAT 600	COMMENT		
QY	681 TTCCACACATAATGAGGAACATTGGGAACTCTGTAACCTGTCATGGTCAT 740	FEATURES		
Db	601 TTCCACACATAATGAGGAACATTGGGAACTCTGTCATGGTCATGGTCAT 660	source		
QY	741 TGCTACTGGAAATCTGAAACCCCTGTCGGCTCATGGTCAT 700			
Db	661 TGCTACTGGAAATCTGAAACCCCTGTCGGCTCATGGTCATGGTCAT 600			
QY	801 GCAGTGAAGACTCATCTACCATCATGATTGTTACTTCCTGACATCCPATAAC 860			
Db	721 GCAGTGAAGACTCATCTACCATCATGATTGTTACTTCCTGACATCCPATAAC 780			
QY	861 ATGTCATCTCCGAAACACTTCGAGGAATTCTGGCTGAGTCAGAGCACC 920			
Db	781 ATGTCATCTCCGAAACACTTCGAGGAATTCTGGCTGAGTCAGAGCACC 840			
QY	921 AGTCAGTGGCAAGGCCAGCACTGGATGACTCTGTCAGGAGACTCTGCGCATC 980			
Db	841 AGTCAGTGGCAAGGCCAGCACTGGATGACTCTGTCAGGAGACTCTGCGCATC 900			
BASE COUNT	255 a 259 C 247 g 322 t	BASE COUNT	255 a 259 C 247 g 322 t	



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